

SEQUENCE LISTING

<110> Hsueh, Aaron
 Hsu, Yu Sheau
 Liang, Shan-Guang
 van der Spek, Petrus Johannes

<120> Novel Mammalian G-Protein Coupled
 Receptors Having Extracellular Leucine Rich Repeat Regions

<130> SUN-84PCT

<160> 8

<170> FastSEQ for Windows Version 3.0

<210> 1
 <211> 2856
 <212> DNA
 <213> human

<400> 1

atgccggggc	cgctagggct	gctctgcttc	ctcgccctgg	ggctgctcgg	ctcgcccggg	60
cccagcgcg	cggcgcgcg	tctctgcgag	gcgccttgca	gctgcgacgg	cgaccgctcg	120
gtggactgct	ccggaaaggg	gttgacggcc	gtaccggagg	gtctcagcgc	cttcacccaa	180
gcactggata	tcagtatgaa	caatatcacc	cagttaccag	aagatgcatt	taagagtttc	240
ccattttctag	aggagctaca	actggctggt	aacgaccttt	ctcttatcca	tccaaaagcc	300
ttgtctgggc	tgaaagaact	caaagtccta	acactccaga	ataatcagtt	gagaacagtg	360
cccagtgaag	ccattcacgg	actgagtgct	ttgcagtcct	tacgcttaga	tgccaacctat	420
attacctcag	tcccggagga	cagttttgaa	gggcttgctc	agttacgcca	tctgtggctg	480
gatgacaaca	gcttgacgga	agtgcgcgtg	cgccccctca	gcaacctgcc	aacctgtcag	540
gcgctgacct	tggtctctcaa	caacatctca	agcatccctg	acttcgcttt	caccaacctt	600
tcaagcttgg	tggttctgca	tctgcataac	aataaaatta	aaagcctcag	tcaacactgt	660
tttgatggac	tagataacct	ggaaaccttg	gacttgaatt	acaattactt	ggatgagttt	720
cctcaggcta	ttaaagccct	tcccagcctt	aaagagctgg	gatttcacag	taattctatt	780
tctgttattc	ctgatggagc	atttggtggt	aatccactgc	taagaactat	tcatttgtat	840
gataatcctc	tgtcttttgt	ggggaactca	gcatttcaca	acctgtctga	tctgcattgc	900
ttagtcattc	gtggtgcaag	cctggtgcag	tggttcccca	atctgaccgg	aactgtccat	960
ttggagagtc	taaccttgac	agggacaaaa	ataagcagca	tacctgatga	tctgtgccaa	1020
aaccaaaaga	tgctgaggac	tctggactta	tcttataaca	atataagaga	ccttccaagt	1080
tttaatgggt	gtcgtgcatt	ggaagaaatt	tcattgcagc	gtaatcaaat	ctccctaata	1140
aaggaaaata	cttttcaagg	cctaacatct	ctaaggattc	tagatctgag	tagaaacctg	1200
atccgtgaaa	ttcacagtgg	agcttttgcg	aagcttgggg	caattactaa	cctggatgta	1260
agtttcaatg	aattaacttc	atttcctacg	gaaggcctaa	atgggctcaa	tcaactaaag	1320
cttgtgggta	acttcaagct	gaaagacgcc	ttggcagcca	gagactttgc	taatctcagg	1380
tctctatcag	taccatatgc	ttatcagtgt	tgtgcatttt	gggggtgtga	ctctttatgc	1440
aaattaaaca	cagaagataa	cagcccccaa	gaacacagtg	tgacaaaaga	gaaagggtgct	1500
acagatgcag	caaatgtcac	cagcactgct	gagaacgaag	aacatagcca	aataattatc	1560
cactgtacac	cttcaacagg	tgctttcaag	ccctgtgaat	atttactggg	aagctggatg	1620
attcgcccta	cagtgtgggt	cattttcctg	gtcgccctgc	ttttcaacct	gcttgtcatt	1680
ttaacagtg	ttgcgtcttg	ttcatcactg	cctgcctcca	aactcttcat	aggcttgatt	1740
tctgtgtcta	acttactcat	gggcatctat	actggcatcc	ttacttttct	tgatgctgtg	1800
tctggggcc	gatttgccga	atttggcatt	tggtgggaaa	ctggcagcgg	ctgcaaggta	1860
gccgggtctc	tggcagtctt	ctcctcagag	agcgctgtat	tcctattaac	actggcagct	1920
gtggaaagaa	gcgtatttgc	aaaggatttg	atgaaacacg	ggaagagcag	tcacctcaga	1980
cagttccagg	tgccgcgcct	cttagctttg	ctgggtgccc	cagtggcagg	ctgcttcccc	2040
cttttccacg	gagggaataa	ttctgcacgc	cccttggtgt	tgccgtttcc	tacaggagaa	2100

```

accccatcgt taggattcac tgtgacctta gtgctattaa actcactggc atttttacta 2160
atggccatta tctacactaa actatactgc aacttagaga aggaggacct gtcggaaaac 2220
tcccagtcga gcgtgattaa gcacgttgcc tggctcatct tcacaaactg catcttcttc 2280
tgccctgttg catttttctc atttgcacca ttgatcacgg caatctccat cagccccgag 2340
ataatgaagt ctgttacact gatattcttc ccgttgccctg cttgcctgaa tccggtcctg 2400
tatgttttct tcaacccaaa gtttaaagaa gactggaagc tactgaagcg gcgtgttacc 2460
aggaaacacg gatctgtttc agtttccatc agcagccaag gcggttggtg ggaacaggat 2520
ttctactatg actgtggcat gtattcccac ttgcagggtg acctgactgt ctgtgactgc 2580
tgtgagtcac ttcttttgac aaaaccagta tcatgcaaac acttaataaa atcgcacagt 2640
tgtcctgtat tgacagcggc ctcttgccag aggccagagg cctactgggtc tgattgtggt 2700
acacagtcag cccattctga ctatgcagat gaagaagatt cctttgtctc agacagctct 2760
gaccaggtgc agcctgtgg acgagcctgc ttctaccaga gtcgtggatt ccctctggtg 2820
cgctatgctt acaatctaca gagagtcaga gactga 2856

```

<210> 2

<211> 951

<212> PRT

<213> human

<400> 2

```

Met Pro Gly Pro Leu Gly Leu Leu Cys Phe Leu Ala Leu Gly Leu Leu
 1          5          10          15
Gly Ser Ala Gly Pro Ser Gly Ala Ala Pro Pro Leu Cys Ala Ala Pro
 20          25          30
Cys Ser Cys Asp Gly Asp Arg Arg Val Asp Cys Ser Gly Lys Gly Leu
 35          40          45
Thr Ala Val Pro Glu Gly Leu Ser Ala Phe Thr Gln Ala Leu Asp Ile
 50          55          60
Ser Met Asn Asn Ile Thr Gln Leu Pro Glu Asp Ala Phe Lys Ser Phe
 65          70          75          80
Pro Phe Leu Glu Glu Leu Gln Leu Ala Gly Asn Asp Leu Ser Leu Ile
 85          90          95
His Pro Lys Ala Leu Ser Gly Leu Lys Glu Leu Lys Val Leu Thr Leu
100          105          110
Gln Asn Asn Gln Leu Arg Thr Val Pro Ser Glu Ala Ile His Gly Leu
115          120          125
Ser Ala Leu Gln Ser Leu Arg Leu Asp Ala Asn His Ile Thr Ser Val
130          135          140
Pro Glu Asp Ser Phe Glu Gly Leu Val Gln Leu Arg His Leu Trp Leu
145          150          155          160
Asp Asp Asn Ser Leu Thr Glu Val Pro Val Arg Pro Leu Ser Asn Leu
165          170          175
Pro Thr Leu Gln Ala Leu Thr Leu Ala Leu Asn Asn Ile Ser Ser Ile
180          185          190
Pro Asp Phe Ala Phe Thr Asn Leu Ser Ser Leu Val Val Leu His Leu
195          200          205
His Asn Asn Lys Ile Lys Ser Leu Ser Gln His Cys Phe Asp Gly Leu
210          215          220
Asp Asn Leu Glu Thr Leu Asp Leu Asn Tyr Asn Tyr Leu Asp Glu Phe
225          230          235          240
Pro Gln Ala Ile Lys Ala Leu Pro Ser Leu Lys Glu Leu Gly Phe His
245          250          255
Ser Asn Ser Ile Ser Val Ile Pro Asp Gly Ala Phe Gly Gly Asn Pro
260          265          270
Leu Leu Arg Thr Ile His Leu Tyr Asp Asn Pro Leu Ser Phe Val Gly
275          280          285
Asn Ser Ala Phe His Asn Leu Ser Asp Leu His Cys Leu Val Ile Arg
290          295          300

```

Gly Ala Ser Leu Val Gln Trp Phe Pro Asn Leu Thr Gly Thr Val His
 305 310 315 320
 Leu Glu Ser Leu Thr Leu Thr Gly Thr Lys Ile Ser Ser Ile Pro Asp
 325 330 335
 Asp Leu Cys Gln Asn Gln Lys Met Leu Arg Thr Leu Asp Leu Ser Tyr
 340 345 350
 Asn Asn Ile Arg Asp Leu Pro Ser Phe Asn Gly Cys Arg Ala Leu Glu
 355 360 365
 Glu Ile Ser Leu Gln Arg Asn Gln Ile Ser Leu Ile Lys Glu Asn Thr
 370 375 380
 Phe Gln Gly Leu Thr Ser Leu Arg Ile Leu Asp Leu Ser Arg Asn Leu
 385 390 395 400
 Ile Arg Glu Ile His Ser Gly Ala Phe Ala Lys Leu Gly Thr Ile Thr
 405 410 415
 Asn Leu Asp Val Ser Phe Asn Glu Leu Thr Ser Phe Pro Thr Glu Gly
 420 425 430
 Leu Asn Gly Leu Asn Gln Leu Lys Leu Val Gly Asn Phe Lys Leu Lys
 435 440 445
 Asp Ala Leu Ala Ala Arg Asp Phe Ala Asn Leu Arg Ser Leu Ser Val
 450 455 460
 Pro Tyr Ala Tyr Gln Cys Cys Ala Phe Trp Gly Cys Asp Ser Leu Cys
 465 470 475 480
 Lys Leu Asn Thr Glu Asp Asn Ser Pro Gln Glu His Ser Val Thr Lys
 485 490 495
 Glu Lys Gly Ala Thr Asp Ala Ala Asn Val Thr Ser Thr Ala Glu Asn
 500 505 510
 Glu Glu His Ser Gln Ile Ile Ile His Cys Thr Pro Ser Thr Gly Ala
 515 520 525
 Phe Lys Pro Cys Glu Tyr Leu Leu Gly Ser Trp Met Ile Arg Leu Thr
 530 535 540
 Val Trp Phe Ile Phe Leu Val Ala Leu Leu Phe Asn Leu Leu Val Ile
 545 550 555 560
 Leu Thr Val Phe Ala Ser Cys Ser Ser Leu Pro Ala Ser Lys Leu Phe
 565 570 575
 Ile Gly Leu Ile Ser Val Ser Asn Leu Leu Met Gly Ile Tyr Thr Gly
 580 585 590
 Ile Leu Thr Phe Leu Asp Ala Val Ser Trp Gly Arg Phe Ala Glu Phe
 595 600 605
 Gly Ile Trp Trp Glu Thr Gly Ser Gly Cys Lys Val Ala Gly Ser Leu
 610 615 620
 Ala Val Phe Ser Ser Glu Ser Ala Val Phe Leu Leu Thr Leu Ala Ala
 625 630 635 640
 Val Glu Arg Ser Val Phe Ala Lys Asp Leu Met Lys His Gly Lys Ser
 645 650 655
 Ser His Leu Arg Gln Phe Gln Val Ala Ala Leu Leu Ala Leu Leu Gly
 660 665 670
 Ala Ala Val Ala Gly Cys Phe Pro Leu Phe His Gly Gly Gln Tyr Ser
 675 680 685
 Ala Ser Pro Leu Cys Leu Pro Phe Pro Thr Gly Glu Thr Pro Ser Leu
 690 695 700
 Gly Phe Thr Val Thr Leu Val Leu Leu Asn Ser Leu Ala Phe Leu Leu
 705 710 715 720
 Met Ala Ile Ile Tyr Thr Lys Leu Tyr Cys Asn Leu Glu Lys Glu Asp
 725 730 735
 Leu Ser Glu Asn Ser Gln Ser Ser Val Ile Lys His Val Ala Trp Leu
 740 745 750
 Ile Phe Thr Asn Cys Ile Phe Phe Cys Pro Val Ala Phe Phe Ser Phe
 755 760 765

Ala Pro Leu Ile Thr Ala Ile Ser Ile Ser Pro Glu Ile Met Lys Ser
 770 775 780
 Val Thr Leu Ile Phe Phe Pro Leu Pro Ala Cys Leu Asn Pro Val Leu
 785 790 795 800
 Tyr Val Phe Phe Asn Pro Lys Phe Lys Glu Asp Trp Lys Leu Leu Lys
 805 810 815
 Arg Arg Val Thr Arg Lys His Gly Ser Val Ser Val Ser Ile Ser Ser
 820 825 830
 Gln Gly Gly Cys Gly Glu Gln Asp Phe Tyr Tyr Asp Cys Gly Met Tyr
 835 840 845
 Ser His Leu Gln Gly Asn Leu Thr Val Cys Asp Cys Cys Glu Ser Phe
 850 855 860
 Leu Leu Thr Lys Pro Val Ser Cys Lys His Leu Ile Lys Ser His Ser
 865 870 875 880
 Cys Pro Val Leu Thr Ala Ala Ser Cys Gln Arg Pro Glu Ala Tyr Trp
 885 890 895
 Ser Asp Cys Gly Thr Gln Ser Ala His Ser Asp Tyr Ala Asp Glu Glu
 900 905 910
 Asp Ser Phe Val Ser Asp Ser Ser Asp Gln Val Gln Ala Cys Gly Arg
 915 920 925
 Ala Cys Phe Tyr Gln Ser Arg Gly Phe Pro Leu Val Arg Tyr Ala Tyr
 930 935 940
 Asn Leu Gln Arg Val Arg Asp
 945 950

<210> 3
 <211> 2082
 <212> DNA
 <213> human

<400> 3

ctacatctcc	ataacaatag	aatccactcc	ctgggaaaga	aatgctttga	tgggctccac	60
agcctagaga	cttttagattt	aaattacaat	aaccttgatg	aattccccac	tgcaattag	120
acactctcca	acttaaagga	actaggattt	catagcaaca	atatcagggtc	gatacctgag	180
aaagcatttg	taggcaaccc	ttctcttatt	acaatacatt	tctatgacaa	tcccatccaa	240
tttgttgga	gatctgcttt	tcaacattta	cctgaactaa	gaacactgac	tctgaatggt	300
gcctcacaaa	taactgaatt	tccctgattta	actggaactg	caaacctgga	gagctctgact	360
ttactggag	cacagatctc	atctcttctc	caaaccgtct	gcaatcagtt	acctaattctc	420
caagtgttag	atctgtctta	caacctatta	gaagatttac	ccagtttttc	agtctgccaa	480
aagcttcaga	aaattgacct	aagacataat	gaaatctacg	aaattaaagt	tgacactttc	540
cagcagttgc	ttagcctccg	atcgctgaat	ttggcttgga	acaaaattgc	tattattcac	600
cccaatgcat	tttccacttt	gccatcccta	ataaagctgg	acctatcgtc	caacctcctg	660
togtcttttc	ctataactgg	gttacatggt	ttaactcact	taaaattaac	aggaaatcat	720
gccttacaga	gctggatata	atctgaaaac	tttccgaaac	tcaaggtnat	agaaatgcct	780
tatgcttacc	agtgtgtgtc	atttgaggatg	tgtgagaatg	cctataagat	ttctaataca	840
tggaataaag	gtgacaacag	cagtatggac	gaccttcata	agaaagatgc	tggaatggtt	900
caggctcaag	atgaacgtga	ccttgaagat	ttcctgcttg	actttgagga	agacctgaaa	960
gcccttcatt	cagtgcagtg	ttcaccttcc	ccaggcccct	tcaaaccctg	tgaacacctg	1020
cttgatggct	ggctgatcag	aattggagtg	tggaccatag	cagttctggc	acttacttgt	1080
aatgcttttg	tgacttcaac	agttttcaga	tcccctctgt	acatttcccc	cattaaactg	1140
ttaattgggg	tcactgcagc	agtgaacatg	ctcacgggag	tctccagtg	cgtgctggct	1200
gggtgtggatg	cgttcacttt	tggcagcttt	gcacgacatg	gtgcctgggtg	ggagaatggg	1260
gttggttgcc	atgtcatttg	ttttttgtcc	atttttgctt	cagaatcatc	tgttttcctg	1320
cttactctgg	cagccctgga	gcgtgggttc	tctgtgaaat	attctgcaaa	atttgaaacg	1380
aaagctccat	tttctagcct	gaaagtaatc	attttgctct	gtgccctgct	ggccttgacc	1440
atggccgcag	ttcccctgct	gggtggcagc	aagtatggcg	cctcccctct	ctgcctgcct	1500
ttgccttttg	gggagccag	caccatgggc	tacatggctg	ctctcatctt	gctcaattcc	1560
ctttgcttcc	tcatgatgac	cattgcctac	accaagctct	actgcaattt	ggacaaggga	1620
gacctggaga	atattttggga	ctgctctatg	gtaaaaacaca	ttgccctggt	gctcttcacc	1680

```

aactgcatcc taaactgccc tgtggctttc ttgtccttct cctctttaat aaaccttaca 1740
tttatcagtc ctgaagtaat taagtttatc ctctgtggtg tagtccact tcctgcatgt 1800
ctcaatcccc ttctctacat cttgttcaat cctcacttta aggaggatct ggtgagcctg 1860
agaaagcaaa cctacgtctg gacaagatca aaacacccaa gcttgatgtc aattaactct 1920
gatgatgtcg aaaaacagtc ctgtgactca actcaagcct tggtaacctt taccagctcc 1980
agcatcactt atgacctgcc tcccagttcc gtgccatcac cagcttatcc agtgactgag 2040
agctgccatc ttctctctgt ggcatttgtc ccattgtctc aa 2082

```

<210> 4
 <211> 693
 <212> PRT
 <213> human

<400> 4

```

Leu His Leu His Asn Asn Arg Ile His Ser Leu Gly Lys Lys Cys Phe
 1          5          10          15
Asp Gly Leu His Ser Leu Glu Thr Leu Asp Leu Asn Tyr Asn Asn Leu
 20          25          30
Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu Ser Asn Leu Lys Glu Leu
 35          40          45
Gly Phe His Ser Asn Asn Ile Arg Ser Ile Pro Glu Lys Ala Phe Val
 50          55          60
Gly Asn Pro Ser Leu Ile Thr Ile His Phe Tyr Asp Asn Pro Ile Gln
 65          70          75          80
Phe Val Gly Arg Ser Ala Phe Gln His Leu Pro Glu Leu Arg Thr Leu
 85          90          95
Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu Phe Pro Asp Leu Thr Gly
100          105          110
Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr Gly Ala Gln Ile Ser Ser
115          120          125
Leu Pro Gln Thr Val Cys Asn Gln Leu Pro Asn Leu Gln Val Leu Asp
130          135          140
Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro Ser Phe Ser Val Cys Gln
145          150          155          160
Lys Leu Gln Lys Ile Asp Leu Arg His Asn Glu Ile Tyr Glu Ile Lys
165          170          175
Val Asp Thr Phe Gln Gln Leu Leu Ser Leu Arg Ser Leu Asn Leu Ala
180          185          190
Trp Asn Lys Ile Ala Ile Ile His Pro Asn Ala Phe Ser Thr Leu Pro
195          200          205
Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn Leu Leu Ser Ser Phe Pro
210          215          220
Ile Thr Gly Leu His Gly Leu Thr His Leu Lys Leu Thr Gly Asn His
225          230          235          240
Ala Leu Gln Ser Trp Ile Ser Ser Glu Asn Phe Pro Glu Leu Lys Val
245          250          255
Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys Ala Phe Gly Val Cys Glu
260          265          270
Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn Lys Gly Asp Asn Ser Ser
275          280          285
Met Asp Asp Leu His Lys Lys Asp Ala Gly Met Phe Gln Ala Gln Asp
290          295          300
Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp Phe Glu Glu Asp Leu Lys
305          310          315          320
Ala Leu His Ser Val Gln Cys Ser Pro Ser Pro Gly Pro Phe Lys Pro
325          330          335
Cys Glu His Leu Leu Asp Gly Trp Leu Ile Arg Ile Gly Val Trp Thr
340          345          350

```

Ile Ala Val Leu Ala Leu Thr Cys Asn Ala Leu Val Thr Ser Thr Val
 355 360 365
 Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile Lys Leu Leu Ile Gly Val
 370 375 380
 Ile Ala Ala Val Asn Met Leu Thr Gly Val Ser Ser Ala Val Leu Ala
 385 390 395 400
 Gly Val Asp Ala Phe Thr Phe Gly Ser Phe Ala Arg His Gly Ala Trp
 405 410 415
 Trp Glu Asn Gly Val Gly Cys His Val Ile Gly Phe Leu Ser Ile Phe
 420 425 430
 Ala Ser Glu Ser Ser Val Phe Leu Leu Thr Leu Ala Ala Leu Glu Arg
 435 440 445
 Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe Glu Thr Lys Ala Pro Phe
 450 455 460
 Ser Ser Leu Lys Val Ile Ile Leu Leu Cys Ala Leu Leu Ala Leu Thr
 465 470 475 480
 Met Ala Ala Val Pro Leu Leu Gly Gly Ser Lys Tyr Gly Ala Ser Pro
 485 490 495
 Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro Ser Thr Met Gly Tyr Met
 500 505 510
 Val Ala Leu Ile Leu Leu Asn Ser Leu Cys Phe Leu Met Met Thr Ile
 515 520 525
 Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp Lys Gly Asp Leu Glu Asn
 530 535 540
 Ile Trp Asp Cys Ser Met Val Lys His Ile Ala Leu Leu Leu Phe Thr
 545 550 555 560
 Asn Cys Ile Leu Asn Cys Pro Val Ala Phe Leu Ser Phe Ser Ser Leu
 565 570 575
 Ile Asn Leu Thr Phe Ile Ser Pro Glu Val Ile Lys Phe Ile Leu Leu
 580 585 590
 Val Val Val Pro Leu Pro Ala Cys Leu Asn Pro Leu Leu Tyr Ile Leu
 595 600 605
 Phe Asn Pro His Phe Lys Glu Asp Leu Val Ser Leu Arg Lys Gln Thr
 610 615 620
 Tyr Val Trp Thr Arg Ser Lys His Pro Ser Leu Met Ser Ile Asn Ser
 625 630 635 640
 Asp Asp Val Glu Lys Gln Ser Cys Asp Ser Thr Gln Ala Leu Val Thr
 645 650 655
 Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu Pro Pro Ser Ser Val Pro
 660 665 670
 Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys His Leu Ser Ser Val Ala
 675 680 685
 Phe Val Pro Cys Leu
 690

<210> 5

<211> 2467

<212> DNA

<213> human

<400> 5

gaaaggagga	aagaaaaaaa	gaggaatgga	aagagacaga	gaaaggaaat	gggagtggaa	60
ggagggagga	ctgctttgta	actgctaaga	ttgcagacag	aaatagcaca	caaccactgt	120
gagctgtatg	cgattcagaa	accaagacca	aattttgctc	actttcatta	atcagttgct	180
cagatagaag	gaaatgacat	ctggttctgt	cttcttctac	atcttaattt	ttggaaaata	240
tttttctcat	gggggtggac	aggatgtcaa	gtgctccctt	ggctatttcc	cctgtgggaa	300
catcacaaag	tgcttgccctc	agctcctgca	ctgtaacggt	gtggacgact	gcgggaatca	360
ggccgatgag	gacaactgtg	gagacaacaa	tggatggtcc	atgcaatttg	acaaatattt	420
tgccagttac	tacaaaatga	cttcccaata	tccttttgag	gcagaaacac	ctgaatgttt	480

```

ggtcggttct gtgccagtgc aatgtctttg ccaaggtctg gagcttgact gtgatgaaac 540
caatttacga gctgttccat cggtttcttc aaatgtgact gcaatgtcac ttcagtggaa 600
cttaataaga aagcttcctc ctgattgctt caagaattat catgatcttc agaagctgta 660
cctgcaaaac aataagatta catccatctc catctatgct ttcagaggac tgaatagcct 720
tactaaactg tatctcagtc ataacagaat aaccttcctg aagccgggtg tttttgaaga 780
tcttcacaga ctagaatggc tgataattga agataatcac ctcagtcgaa tttccccacc 840
aacattttat ggactaaatt ctcttattct cttagtctct atgaataacg tcctcaccgc 900
tttacctgat aaacctctct gtcaacacat gccaaagact cattggctgg accttgaagg 960
caaccatata cataatttaa gaaatttgac ttttatttcc tgcagtaatt taactgtttt 1020
agtgatgagg aaaaacaaaa ttaatcactt aaatgaaaat acttttgcac ctctccagaa 1080
actggatgaa ttggatttag gaagtaataa gattgaaaat cttccaccgc ttatattcaa 1140
ggacctgaag gagctgtcac aattgaatct ttcctataat ccaatccaga aaattcaagc 1200
aaaccaattt gattatcttg tcaaatcaa gtctctcagc ctagaaggga ttgaaatttc 1260
aaatatccaa caaaggatgt ttagacctct tatgaatctc tctcacatat attttaagaa 1320
attccagtac tgtgggtatg caccacatgt tcgcagctgt aaaccaaaca ctgatggaat 1380
ttcatctcta gagaatctct tggcaagcat tattcagaga gtatttgtct gggttgtatc 1440
tgcagttacc tgctttggaa acatttttgc catttgcatt cgaccttata tcaggtctga 1500
gaacaagctg tatgccatgt caatcatttc tctctgctgt gccgactgct taatgggaat 1560
atatttattc gtgatcggag gctttgacct aaagtctcgt ggagaatata ataagcatgc 1620
gcagctgtgg atggagagta ctcattgtca gcttgtagga tctttggcca ttctgtccac 1680
agaagtatca gttttactgt taacatttct gacattggaa aaatacatct gcattgtcta 1740
tcctttttaga tgtgtgagac ctggaaaatg cagaacaatt acagttctga ttctcatttg 1800
gattactggg tttatagtgg ctttcattcc attgagcaat aaggaatttt tcaaaaacta 1860
ctatggcacc aatggagtat gcttccctct tcattcagaa gatacagaaa gtattggagc 1920
ccagatttat tcagtggaaca tttttcttgg tattaatttg gccgcattta tcatcatagt 1980
tttttctat ggaagcatgt tttatagtgt tcataaaagt gccataacag caactgaaat 2040
acggaatcaa gttaaaaaag agatgatcct tgccaaaact ctttcttcta tagtatttac 2100
tgatgcatta tgctggatac ccatttttgt agtgaaaatt ctttctactg ttcaggtaga 2160
aataccaggt accataacct cttgggtagt gatttttatt ctgccatta acagtgtctt 2220
gaacccaatt ctctatactc tgaccacaag accatttaaa gaaatgattc atcggttttg 2280
gtataactac agacaaagaa aatctatgga cagcaaaggc cagaaaacat atgctccatc 2340
attcatctgg gtggaaatgt ggccactgca ggagatgcca cctgagttaa tgaagccgga 2400
ccttttcaca taccctgtgt aaatgtcact gatttctcaa tcaacgagac tcaattocta 2460
ttcatga 2467

```

<210> 6
 <211> 757
 <212> PRT
 <213> human

<400> 6

Met	Thr	Ser	Gly	Ser	Val	Phe	Phe	Tyr	Ile	Leu	Ile	Phe	Gly	Lys	Tyr
1				5					10					15	
Phe	Ser	His	Gly	Gly	Gly	Gln	Asp	Val	Lys	Cys	Ser	Leu	Gly	Tyr	Phe
			20					25					30		
Pro	Cys	Gly	Asn	Ile	Thr	Lys	Cys	Leu	Pro	Gln	Leu	Leu	His	Cys	Asn
		35					40					45			
Gly	Val	Asp	Asp	Cys	Gly	Asn	Gln	Ala	Asp	Glu	Asp	Asn	Cys	Gly	Asp
	50					55					60				
Asn	Asn	Gly	Trp	Ser	Met	Gln	Phe	Asp	Lys	Tyr	Phe	Ala	Ser	Tyr	Tyr
65					70					75				80	
Lys	Met	Thr	Ser	Gln	Tyr	Pro	Phe	Glu	Ala	Glu	Thr	Pro	Glu	Cys	Leu
				85					90					95	
Val	Gly	Ser	Val	Pro	Val	Gln	Cys	Leu	Cys	Gln	Gly	Leu	Glu	Leu	Asp
			100					105					110		
Cys	Asp	Glu	Thr	Asn	Leu	Arg	Ala	Val	Pro	Ser	Val	Ser	Ser	Asn	Val
		115					120					125			
Thr	Ala	Met	Ser	Leu	Gln	Trp	Asn	Leu	Ile	Arg	Lys	Leu	Pro	Pro	Asp
	130					135						140			

Cys Phe Lys Asn Tyr His Asp Leu Gln Lys Leu Tyr Leu Gln Asn Asn
 145 150 155 160
 Lys Ile Thr Ser Ile Ser Ile Tyr Ala Phe Arg Gly Leu Asn Ser Leu
 165 170 175
 Thr Lys Leu Tyr Leu Ser His Asn Arg Ile Thr Phe Leu Lys Pro Gly
 180 185 190
 Val Phe Glu Asp Leu His Arg Leu Glu Trp Leu Ile Ile Glu Asp Asn
 195 200 205
 His Leu Ser Arg Ile Ser Pro Pro Thr Phe Tyr Gly Leu Asn Ser Leu
 210 215 220
 Ile Leu Leu Val Leu Met Asn Asn Val Leu Thr Arg Leu Pro Asp Lys
 225 230 235 240
 Pro Leu Cys Gln His Met Pro Arg Leu His Trp Leu Asp Leu Glu Gly
 245 250 255
 Asn His Ile His Asn Leu Arg Asn Leu Thr Phe Ile Ser Cys Ser Asn
 260 265 270
 Leu Thr Val Leu Val Met Arg Lys Asn Lys Ile Asn His Leu Asn Glu
 275 280 285
 Asn Thr Phe Ala Pro Leu Gln Lys Leu Asp Glu Leu Asp Leu Gly Ser
 290 295 300
 Asn Lys Ile Glu Asn Leu Pro Pro Leu Ile Phe Lys Asp Leu Lys Glu
 305 310 315 320
 Leu Ser Gln Leu Asn Leu Ser Tyr Asn Pro Ile Gln Lys Ile Gln Ala
 325 330 335
 Asn Gln Phe Asp Tyr Leu Val Lys Leu Lys Ser Leu Ser Leu Glu Gly
 340 345 350
 Ile Glu Ile Ser Asn Ile Gln Gln Arg Met Phe Arg Pro Leu Met Asn
 355 360 365
 Leu Ser His Ile Tyr Phe Lys Lys Phe Gln Tyr Cys Gly Tyr Ala Pro
 370 375 380
 His Val Arg Ser Cys Lys Pro Asn Thr Asp Gly Ile Ser Ser Leu Glu
 385 390 395 400
 Asn Leu Leu Ala Ser Ile Ile Gln Arg Val Phe Val Trp Val Val Ser
 405 410 415
 Ala Val Thr Cys Phe Gly Asn Ile Phe Val Ile Cys Met Arg Pro Tyr
 420 425 430
 Ile Arg Ser Glu Asn Lys Leu Tyr Ala Met Ser Ile Ile Ser Leu Cys
 435 440 445
 Cys Ala Asp Cys Leu Met Gly Ile Tyr Leu Phe Val Ile Gly Gly Phe
 450 455 460
 Asp Leu Lys Phe Arg Gly Glu Tyr Asn Lys His Ala Gln Leu Trp Met
 465 470 475 480
 Glu Ser Thr His Cys Gln Leu Val Gly Ser Leu Ala Ile Leu Ser Thr
 485 490 495
 Glu Val Ser Val Leu Leu Leu Thr Phe Leu Thr Leu Glu Lys Tyr Ile
 500 505 510
 Cys Ile Val Tyr Pro Phe Arg Cys Val Arg Pro Gly Lys Cys Arg Thr
 515 520 525
 Ile Thr Val Leu Ile Leu Ile Trp Ile Thr Gly Phe Ile Val Ala Phe
 530 535 540
 Ile Pro Leu Ser Asn Lys Glu Phe Phe Lys Asn Tyr Tyr Gly Thr Asn
 545 550 555 560
 Gly Val Cys Phe Pro Leu His Ser Glu Asp Thr Glu Ser Ile Gly Ala
 565 570 575
 Gln Ile Tyr Ser Val Ala Ile Phe Leu Gly Ile Asn Leu Ala Ala Phe
 580 585 590
 Ile Ile Ile Val Phe Ser Tyr Gly Ser Met Phe Tyr Ser Val His Gln
 595 600 605

Ser Ala Ile Thr Ala Thr Glu Ile Arg Asn Gln Val Lys Lys Glu Met
 610 615 620
 Ile Leu Ala Lys Arg Phe Phe Phe Ile Val Phe Thr Asp Ala Leu Cys
 625 630 635 640
 Trp Ile Pro Ile Phe Val Val Lys Phe Leu Ser Leu Leu Gln Val Glu
 645 650 655
 Ile Pro Gly Thr Ile Thr Ser Trp Val Val Ile Phe Ile Leu Pro Ile
 660 665 670
 Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Arg Pro Phe
 675 680 685
 Lys Glu Met Ile His Arg Phe Trp Tyr Asn Tyr Arg Gln Arg Lys Ser
 690 695 700
 Met Asp Ser Lys Gly Gln Lys Thr Tyr Ala Pro Ser Phe Ile Trp Val
 705 710 715 720
 Glu Met Trp Pro Leu Gln Glu Met Pro Pro Glu Leu Met Lys Pro Asp
 725 730 735
 Leu Phe Thr Tyr Pro Cys Glu Met Ser Leu Ile Ser Gln Ser Thr Arg
 740 745 750
 Leu Asn Ser Tyr Ser
 755

<210> 7
 <211> 3584
 <212> DNA
 <213> human

<400> 7
 ctgcttttcta actgctaaga ttgcagacag aaatagcaca caaccactgt gagctgtatg 60
 cgattcagaa accaagacca aatttttgctc acttttcatta atcagttgct cagatagaag 120
 gaaatgacat ctggttctgt cttcttctac atcttaattt ttggaaaata tttttctcat 180
 gggggtggac aggatgtcaa gtgctccctt ggctatttcc cctgtgggaa catcacaaaag 240
 tgcttgctc agctcctgca ctgtaacggt gtggacgact gcgggaatca ggccgatgag 300
 gacaactgtg tgggtggttt gtgccagtgc atgtctttgc cagggtctgga gcttgactgg 360
 atgaaaccat ttacgagtgt tccatcggtt tcttcaaagt tgactgcaat gtcacttcag 420
 tggaaactta taagaaagct tccctctgat tgcttcaaga attatcatga tcttcagaag 480
 ctggacctgc aaaacaataa gattacatcc atctccatct atgctttcag aggactgaat 540
 agccttacta aactgtatct cagtcataac agaataacct tcctgaagcc ggggtgtttt 600
 gaagatcttc acagactaga atggctgata attgaagata atcacctcag tcgaatttcc 660
 ccaccaacat tttatggact aaattctctt attctcttag tctgatgaa taacgtcctc 720
 acccgtttac ctgataaacc tctctgtcaa cacatgccaa gactacattg gctggacctt 780
 gaaggcaacc atatccataa ttttaagaaat ttgactttta tttcctgcag taatttaact 840
 gtttttagtga tgaggaaaaa caaaattaat cacttaaatg aaaatacttt tgcacctctc 900
 cagaaactgg atgaattgga tttagggaagt aataagattg aaaatcttcc accgcttata 960
 ttcaaggacc tgaaggagct gtcacaattg aatctttcct ataatccaat ccagaaaatt 1020
 caagcaaacc aatttgatta tcttgtcaaa ctcaagtctc tcagcctaga agggattgaa 1080
 atttcaaata tccaacaaag gatgtttaga cctcttatga atctctctca catatatatt 1140
 aagaaattcc agtactgtgg gtatgcacca catgttcgca gctgtaaaacc aaacactgat 1200
 ggaatttcat ctctagagaa tctcttgga agcattatc agagagtatt tgtctgggtt 1260
 gtatctgcag ttacctgctt tggaaacatt tttgtcatt gcacgcgacc ttatatcagg 1320
 tctgagaaca agctgtatgc catgtcaatc atttctctc gctgtgccga ctgcttaattg 1380
 ggaatatatt tattcgtgat cggaggcttt gacctaaagt ttcgtggaga atacaataag 1440
 catgcgcagc tgtggatgga gagtactcat tgtcagcttg taggatcttt ggccattctg 1500
 tccacagaag tatcagtttt actgttaaca tttctgacat tggaaaaata catctgcatt 1560
 gtctatcctt ttagatgtgt gagacctgga aaatgcagaa caattacagt tctgattctc 1620
 atttgagatta ctggttttat agtggctttc attccattga gcaataagga atttttcaaa 1680
 aactactatg gcaccaatgg agtatgett cctcttcatt cagaagatac agaaagtatt 1740
 ggagcccaga tttatttcagt ggcaattttt cttgggtatta atttgccgc atttatcatc 1800
 atagtttttt cctatggaag catgttttat agtgttcac aaagtgccat aacagcaact 1860
 gaaatcacga atcaagttaa aaaagagatg atccttgcca aacgtttttt ctttatagta 1920

```

tttactgatg cattatgctg gataccatt tttgtagtga aatttctttc actgcttcag 1980
gtagaaatac caggtacat aacctcttgg gtagtgattt ttattctgcc catataacagt 2040
gctttgaacc caattctcta tactctgacc acaagacat ttaaagaaat gattcatcgg 2100
ttttggtata actacagaca aagaaaatct atggacagca aaggtcagaa aacatatgct 2160
ccatcattca tctgggtgga aatgtggcca ctgcaggaga tggcacctga gttaatgaag 2220
ccggaccttt tcacataccc ctgtgaaatg tcaactgattt ctcaatcaac gagactcaat 2280
tcctattcat gactgactct gaaattcatt tcttcgcaga gaatactgtg ggggtgcttc 2340
atgaggggatt tactggtatg aaaatgaata ccacaaaatt aatttataat aatagctaag 2400
ataaatatatt tacaaggaca tgaggaaaaa taaaaatgac taatgctctt acaaagggaa 2460
gtaattatat caataatgta tatatattag tagacatttt gcataagaaa ttaagagaaa 2520
tctacttcag taacattcat tcatttttct aacatgcatt tattgagtac ccactactat 2580
gtgcatagca ttgcaatata gtcctggaag tagacagtgc agaacctttc aatctgtaga 2640
tagtgtttaa tgacaaaaga ctatacaaa gtcctctgca gttcctagtt taaagtagag 2700
ctttacctgt catgtgcatc agcaagaatc ataggcactt ttaaataaa gtttaaagtt 2760
ttggaatact cagtgtattt gcatcataga aaatgtctga ctgtttgcaa aataatatte 2820
tgttttaaga atccatctta cctctcttta agtttccata cacttgagag ccaacacaa 2880
atatttatta ctaaaaagat gctttgctag aaactcaaaa acagcacttc ttttggcact 2940
tcctgcccag ttttctcttt gctttaaatg aacatcatca tatggaattg gaataggaga 3000
gtatgagtac ggcagagaag tggatcagaa aaactagaat gaggataaac atttacatta 3060
gtggaaaactc ctgaaataaa tccttgtatt gtcagttaac tgattttcaa caaggatgcc 3120
aagacaaaaa ggcttttcaa caaacctgac tggttttaaga acagacctaa gtggtttaat 3180
tcacccactt tagatgggtg aatgttatgg tgtgtgaaat atctcagtaa agcagttaaa 3240
aggaaaaaga gctggaatgc actgattcag gaacttaatt tcaggaagga aaggtctgta 3300
tgtacacatt tcactttaag cagaaaaatc ttcttcaaga aatgacttta ctttctcttt 3360
gcaactgccag cacgtgagat actaaacttt taactagttg ttcttctcta gtctctacgt 3420
tattagnatt ttttgctttc ataatgtgaa acctttaagc aggagaagaa aatgttttca 3480
gatagtttca aatacnccaa aaatgtttgc aacacaaaaa tactggaatc naaccataat 3540
gcccttattg aatatatagt tgtatagntt tgttctgaaa accc 3584

```

<210> 8

<211> 722

<212> PRT

<213> human

<400> 8

```

Met Thr Ser Gly Ser Val Phe Phe Tyr Ile Leu Ile Phe Gly Lys Tyr
1          5          10          15
Phe Ser His Gly Gly Gly Gln Asp Val Lys Cys Ser Leu Gly Tyr Phe
20        25        30
Pro Cys Gly Asn Ile Thr Lys Cys Leu Pro Gln Leu Leu His Cys Asn
35        40        45
Gly Val Asp Asp Cys Gly Asn Gln Ala Asp Glu Asp Asn Cys Val Val
50        55        60
Val Leu Cys Gln Cys Met Ser Leu Pro Gly Leu Glu Leu Asp Trp Met
65        70        75        80
Lys Pro Phe Thr Ser Val Pro Ser Val Ser Ser Asn Val Thr Ala Met
85        90        95
Ser Leu Gln Trp Asn Leu Ile Arg Lys Leu Pro Pro Asp Cys Phe Lys
100       105       110
Asn Tyr His Asp Leu Gln Lys Leu Asp Leu Gln Asn Asn Lys Ile Thr
115       120       125
Ser Ile Ser Ile Tyr Ala Phe Arg Gly Leu Asn Ser Leu Thr Lys Leu
130       135       140
Tyr Leu Ser His Asn Arg Ile Thr Phe Leu Lys Pro Gly Val Phe Glu
145       150       155       160
Asp Leu His Arg Leu Glu Trp Leu Ile Ile Glu Asp Asn His Leu Ser
165       170       175
Arg Ile Ser Pro Thr Phe Tyr Gly Leu Asn Ser Leu Ile Leu Leu
180       185       190

```

Val	Leu	Met	Asn	Asn	Val	Leu	Thr	Arg	Leu	Pro	Asp	Lys	Pro	Leu	Cys
		195					200					205			
Gln	His	Met	Pro	Arg	Leu	His	Trp	Leu	Asp	Leu	Glu	Gly	Asn	His	Ile
	210					215					220				
His	Asn	Leu	Arg	Asn	Leu	Thr	Phe	Ile	Ser	Cys	Ser	Asn	Leu	Thr	Val
225					230					235					240
Leu	Val	Met	Arg	Lys	Asn	Lys	Ile	Asn	His	Leu	Asn	Glu	Asn	Thr	Phe
				245					250					255	
Ala	Pro	Leu	Gln	Lys	Leu	Asp	Glu	Leu	Asp	Leu	Gly	Ser	Asn	Lys	Ile
			260				265						270		
Glu	Asn	Leu	Pro	Pro	Leu	Ile	Phe	Lys	Asp	Leu	Lys	Glu	Leu	Ser	Gln
	275						280					285			
Leu	Asn	Leu	Ser	Tyr	Asn	Pro	Ile	Gln	Lys	Ile	Gln	Ala	Asn	Gln	Phe
	290					295					300				
Asp	Tyr	Leu	Val	Lys	Leu	Lys	Ser	Leu	Ser	Leu	Glu	Gly	Ile	Glu	Ile
305					310					315					320
Ser	Asn	Ile	Gln	Gln	Arg	Met	Phe	Arg	Pro	Leu	Met	Asn	Leu	Ser	His
				325					330					335	
Ile	Tyr	Phe	Lys	Lys	Phe	Gln	Tyr	Cys	Gly	Tyr	Ala	Pro	His	Val	Arg
		340					345						350		
Ser	Cys	Lys	Pro	Asn	Thr	Asp	Gly	Ile	Ser	Ser	Leu	Glu	Asn	Leu	Leu
		355					360					365			
Ala	Ser	Ile	Ile	Gln	Arg	Val	Phe	Val	Trp	Val	Val	Ser	Ala	Val	Thr
	370					375					380				
Cys	Phe	Gly	Asn	Ile	Phe	Val	Ile	Cys	Met	Arg	Pro	Tyr	Ile	Arg	Ser
385					390					395					400
Glu	Asn	Lys	Leu	Tyr	Ala	Met	Ser	Ile	Ile	Ser	Leu	Cys	Cys	Ala	Asp
			405						410					415	
Cys	Leu	Met	Gly	Ile	Tyr	Leu	Phe	Val	Ile	Gly	Gly	Phe	Asp	Leu	Lys
		420					425						430		
Phe	Arg	Gly	Glu	Tyr	Asn	Lys	His	Ala	Gln	Leu	Trp	Met	Glu	Ser	Thr
		435					440					445			
His	Cys	Gln	Leu	Val	Gly	Ser	Leu	Ala	Ile	Leu	Ser	Thr	Glu	Val	Ser
	450					455					460				
Val	Leu	Leu	Leu	Thr	Phe	Leu	Thr	Leu	Glu	Lys	Tyr	Ile	Cys	Ile	Val
465					470					475					480
Tyr	Pro	Phe	Arg	Cys	Val	Arg	Pro	Gly	Lys	Cys	Arg	Thr	Ile	Thr	Val
			485						490					495	
Leu	Ile	Leu	Ile	Trp	Ile	Thr	Gly	Phe	Ile	Val	Ala	Phe	Ile	Pro	Leu
			500					505					510		
Ser	Asn	Lys	Glu	Phe	Phe	Lys	Asn	Tyr	Tyr	Gly	Thr	Asn	Gly	Val	Cys
		515					520					525			
Phe	Pro	Leu	His	Ser	Glu	Asp	Thr	Glu	Ser	Ile	Gly	Ala	Gln	Ile	Tyr
	530					535					540				
Ser	Val	Ala	Ile	Phe	Leu	Gly	Ile	Asn	Leu	Ala	Ala	Phe	Ile	Ile	Ile
545					550					555					560
Val	Phe	Ser	Tyr	Gly	Ser	Met	Phe	Tyr	Ser	Val	His	Gln	Ser	Ala	Ile
			565						570					575	
Thr	Ala	Thr	Glu	Ile	Arg	Asn	Gln	Val	Lys	Lys	Glu	Met	Ile	Leu	Ala
			580					585					590		
Lys	Arg	Phe	Phe	Phe	Ile	Val	Phe	Thr	Asp	Ala	Leu	Cys	Trp	Ile	Pro
		595					600					605			
Ile	Phe	Val	Val	Lys	Phe	Leu	Ser	Leu	Leu	Gln	Val	Glu	Ile	Pro	Gly
	610					615					620				
Thr	Ile	Thr	Ser	Trp	Val	Val	Ile	Phe	Ile	Leu	Pro	Ile	Asn	Ser	Ala
625					630					635					640
Leu	Asn	Pro	Ile	Leu	Tyr	Thr	Leu	Thr	Thr	Arg	Pro	Phe	Lys	Glu	Met
			645						650					655	

Ile His Arg Phe Trp Tyr Asn Tyr Arg Gln Arg Lys Ser Met Asp Ser
660 665 670
Lys Gly Gln Lys Thr Tyr Ala Pro Ser Phe Ile Trp Val Glu Met Trp
675 680 685
Pro Leu Gln Glu Met Pro Pro Glu Leu Met Lys Pro Asp Leu Phe Thr
690 695 700
Tyr Pro Cys Glu Met Ser Leu Ile Ser Gln Ser Thr Arg Leu Asn Ser
705 710 715 720
Tyr Ser